AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.

LISTING OF CLAIMS

1. (previously presented) A method for identifying a search model to use in molecular replacement for determining a structure of a target biomolecule from crystal data, the method comprising:

employing first computer executable logic to perform multiple molecular replacement searches on crystal data of the target biomolecule where a group of structures of different biomolecules are used as search models for the multiple molecular replacement searches; and

employing second computer executable logic to compare the molecular replacement solutions produced by the first computer executable logic, the comparison producing data that predicts which biomolecule structures in the group have superior structural identity with the target biomolecule as compared to the other biomolecule structures in the group.

2. (original) A method according to claim 1 wherein comparing molecular replacement solutions comprises comparing figures of merit calculated for the molecular replacement solutions.

3. (previously presented) A method according to claim 2 wherein comparing molecular replacement solutions comprises performing a statistical analysis on figures of merit calculated for the molecular replacement solutions.

4. (previously presented) A method according to claim 2 wherein comparing molecular replacement solutions comprises determining which of the biomolecule structures in the group produced a molecular replacement solution whose figure of merit

is at least two standard deviations better than the average figure of merit for molecular replacement solutions for the biomolecule structures in the group.

5. (previously presented) A method according to claim 2 wherein comparing molecular replacement solutions comprises determining which of the biomolecule structures in the group produced a molecular replacement solution whose figure of merit is at least three standard deviations better than the average figure of merit for molecular replacement solutions for the biomolecule structures in the group.

6. (previously presented) A method according to claim 2 wherein comparing molecular replacement solutions comprises determining which of the biomolecule structures in the group produced a molecular replacement solution whose figure of merit is at least five standard deviations better than the average figure of merit for molecular replacement solutions for the biomolecule structures in the group.

7. (previously presented) A method according to claim 2 wherein comparing molecular replacement solutions comprises determining which of the biomolecule structures in the group produced a molecular replacement solution whose figure of merit is at least ten standard deviations better than the average figure of merit for molecular replacement solutions for the biomolecule structures in the group.

8. (original) A method according to claim 1 wherein comparing molecular replacement solutions comprises comparing root mean square errors for each molecular replacement solution of a probability-weighted average over all possible phase choices.

9. (original) A method according to claim 1 wherein comparing molecular replacement solutions comprises establishing a background correlation level between the biomolecule structures in the group and the target biomolecule based on the molecular replacement solutions and determining which of the biomolecule structures in

the group produced a molecular replacement solution that exceeds the background correlation level by at least two standard deviations.

10. (original) A method according to claim 1 wherein comparing molecular replacement solutions comprises establishing a background correlation level between the biomolecule structures in the group and the target biomolecule based on the molecular replacement solutions and determining which of the biomolecule structures in the group produced a molecular replacement solution that exceeds the background correlation level by at least three standard deviations.

11. (original) A method according to claim 1 wherein comparing molecular replacement solutions comprises establishing a background correlation level between the biomolecule structures in the group and the target biomolecule based on the molecular replacement solutions and determining which of the biomolecule structures in the group produced a molecular replacement solution that exceeds the background correlation level by at least five standard deviations.

12. (original) A method according to claim 1 wherein comparing molecular replacement solutions comprises establishing a background correlation level between the biomolecule structures in the group and the target biomolecule based on the molecular replacement solutions and determining which of the biomolecule structures in the group produced a molecular replacement solution that exceeds the background correlation level by at least ten standard deviations.

13. (currently amended) A method according to claim ~~2~~ 1 wherein the group of different biomolecule structures on which molecular replacement searches are performed comprises at least 3 different biomolecule structures.

14. (currently amended) A method according to claim ~~2~~ 1 wherein the group of different biomolecule structures on which molecular replacement searches are

performed comprises at least 0.1% of the protein structures stored in the Protein Data Bank.

15. (currently amended) A method according to claim ~~2~~ 1 wherein the group of different biomolecule structures on which molecular replacement searches are performed comprises at least one biomolecule structure that has less than 70% sequence identity with the target biomolecule.

16. (currently amended) A method according to claim ~~2~~ 1 wherein the group of different biomolecule structures on which molecular replacement searches are performed comprises structures of at least two different biomolecules that are sufficiently structurally dissimilar to each other that the structure of the at least two different biomolecules would not both be effective search models for a same target molecule.

17. (currently amended) A method according to claim ~~2~~ 1 wherein the group of different biomolecule structures on which molecular replacement searches are performed comprises at least two different biomolecule structures that have less than 70% sequence identity with each other.

18. (currently amended) A method according to claim ~~2~~ 1 wherein the group of different biomolecule structures on which molecular replacement searches are performed comprises at least one predicted structure for a biomolecule.

19. (currently amended) A method according to claim ~~2~~ 1 wherein the group of different biomolecule structures on which molecular replacement searches are performed comprises at least one structure where at least a portion of the native structure has been removed.

20. (currently amended) A method according to claim ~~2~~ 1 wherein the group of different biomolecule structures on which molecular replacement searches are performed comprises at least one structure which comprises a combination of two or more structure fragments.

21. (previously presented) A method according to claim 1 wherein the data produced from the comparison identifies which biomolecule structures produced molecular replacement solutions that have a figure of merit at least among the top 35% of molecular replacement solutions produced by the group.

22. (previously presented) A method according to claim 1 wherein the data produced from the comparison identifies which biomolecule structures produced molecular replacement solutions have a figure of merit that is at least two standard deviations better than the molecular replacement solutions produced by the group.

23. (previously presented) A method according to claim 1 wherein the data produced from the comparison identifies which biomolecule structures produced molecular replacement solutions have a figure of merit that is at least three standard deviations better than the molecular replacement solutions produced by the group.

24. (previously presented) A method according to claim 1 wherein the data produced from the comparison identifies which biomolecule structures produced molecular replacement solutions have a figure of merit that is at least five standard deviations better than the molecular replacement solutions produced by the group.

25. (previously presented) A method according to claim 1 wherein the data produced from the comparison identifies which biomolecule structures produced molecular replacement solutions have a figure of merit that is at least ten standard deviations better than the molecular replacement solutions produced by the group.

26. (original) A method according to claim 1, further comprising employing computer executable logic to select the group of different biomolecule structures used to perform the multiple molecular replacement searches.

27. (original) A method according to claim 26 wherein selection of the group of biomolecule structures is based, at least in part, on sequence identity between the biomolecule structure and the target biomolecule.

28. (original) A method according to claim 26 wherein selection of the group of biomolecule structures is at least partially random.

29. (original) A method according to claim 26 wherein selection of the group of biomolecule structures is completely random.

30. (original) A method according to claim 26 wherein selection of the group of biomolecule structures is iterative.

31. (original) A method according to claim 26 wherein selection of members of the group of biomolecule structures is performed until a biomolecule structure is selected whose molecular replacement solution is at least two standard deviations better than the average molecular replacement solution for the biomolecule structures in the group.

32. (original) A method according to claim 26 wherein selection of members of the group of biomolecule structures is performed until a biomolecule structure is selected whose molecular replacement solution is at least three standard deviations better than the average molecular replacement solution for the biomolecule structures in the group.

33. (original) A method according to claim 26 wherein selection of members of the group of biomolecule structures is performed until a biomolecule structure is selected whose molecular replacement solution is at least five standard deviations better than the average molecular replacement solution for the biomolecule structures in the group.

34. (original) A method according to claim 26 wherein selection of members of the group of biomolecule structures is performed until a biomolecule structure is selected whose molecular replacement solution is at least ten standard deviations better than the average molecular replacement solution for the biomolecule structures in the group.

35. (original) A method according to claim 26 wherein selection of the group of biomolecule structures comprises selecting at least 0.1% of the structures stored in the Protein Data Bank.

36. (original) A method according to claim 1 wherein selection of the group of biomolecule structures comprises selecting at least one biomolecule structure that has less than 70% sequence identity with the target biomolecule.

37. (original) A method according to claim 1 wherein selection of the group of biomolecule structures comprises selecting at least two biomolecule structures that are structurally dissimilar.

38. (original) A method according to claim 1 wherein selection of the group of biomolecule structures comprises selecting at least two biomolecule structures that have less than 70% sequence identity with each other.

39. (original) A method according to claim 1 wherein molecular replacement is performed using a program selected from the group consisting of AMoRe, BRUTE,

COMO, wARP, molREP, EPMR, XPLOR, CNS, TNT, GLRF, TRANSF, TF, ENVELOPE, FFSYNTH, FFTINV, FFTEXP, and RECIP.

40. (original) A method according to claim 1 wherein molecular replacement is performed using EPMR.

41. (original) A method according to claim 1 wherein molecular replacement is performed using a molecular replacement program comprising an evolutionary algorithm for searching six-dimensional space.

42. (original) A method according to claim 1 wherein the biomolecule is a protein.

43. (original) A method according to claim 1 wherein the biomolecule is a DNA.

44. (original) A method according to claim 1 wherein the biomolecule is a RNA.

45. (original) A method according to claim 1 wherein the biomolecule is a complex comprising a protein.

46. (original) A method according to claim 1 wherein the biomolecule is a complex comprising DNA.

47. (original) A method according to claim 1 wherein the biomolecule is a complex comprising RNA.

48. (original) A method according to claim 1 wherein the crystal data is X-ray diffraction data.

49. (original) A method according to claim 1 wherein the crystal data is neutron diffraction crystal data.

50. (original) A method according to claim 1 wherein the crystal data is nuclear magnetic resonance crystal data.

51. (original) A method according to claim 1 wherein the crystal data is mass spectroscopy crystal data.

52. (previously presented) A computer readable medium useful in association with a computer which includes a processor and a memory, the computer readable medium comprising:

first logic for performing multiple molecular replacement searches on crystal data of a target biomolecule where a group of structures of different biomolecules are used as search models for the multiple molecular replacement searches; and

second logic which takes results of the multiple molecular replacement searches performed by the first logic and compares solutions from the multiple molecular replacement searches, the comparison producing data that predicts which biomolecule structures from the group have superior structural identity with the target biomolecule as compared to the other biomolecule structures in the group.

53. (previously presented) A method for identifying a search model to use in molecular replacement for determining a structure of a target biomolecule from crystal data, the method comprising:

employing first computer executable logic to perform multiple molecular replacement searches on crystal data of the target biomolecule where a group of structures of different biomolecules are used as search models for the multiple molecular replacement searches; and

employing second computer executable logic to predict based on the molecular replacement solutions produced by the first computer executable logic a biomolecule structure from the group whose use as a search model will produce a molecular replacement solution that is superior to the molecular replacement solutions produced by the other biomolecule structures in the group.

54. (previously presented) A computer readable medium useful in association with a computer which includes a processor and a memory, the computer readable medium comprising:

first logic for performing multiple molecular replacement searches on X-ray diffraction data of a target biomolecule where a group of structures of different biomolecules are used as search models for the multiple molecular replacement searches; and

second logic which takes results of the multiple molecular replacement searches performed by the first logic and predicts which biomolecule structure from the group whose use as a search model will produce a molecular replacement solution that is superior to the molecular replacement solutions produced by the other biomolecule structures in the group.

55. (previously presented) A method for determining a structure of a target biomolecule from crystal data, the method comprising:

employing first computer executable logic to perform multiple molecular replacement searches on crystal data of the target biomolecule where a group of structures of different biomolecules are used as search models for the multiple molecular replacement searches;

employing second computer executable logic to predict based on the molecular replacement solutions produced by the first computer executable logic a biomolecule structure from the group whose use as a search model will produce a molecular replacement solution that is superior to the molecular replacement solutions produced by the other biomolecule structures in the group; and

employing computer executable logic to determine a structure for the target biomolecule employing the identified biomolecule structure.

56. (previously presented) A computer readable medium useful in association with a computer which includes a processor and a memory, the computer readable medium comprising:

first logic for performing multiple molecular replacement searches on crystal data of a target biomolecule where a group of structures of different biomolecules are used as search models for the multiple molecular replacement searches;

second logic which takes results of the multiple molecular replacement searches performed by the first logic and predicts which biomolecule structure from the group whose use as a search model will produce a molecular replacement solution that is superior to the molecular replacement solutions produced by the other biomolecule structures in the group; and

third logic for determining a structure for the target biomolecule employing the identified biomolecule structure.

57. (previously presented) A method for identifying a search model to use in molecular replacement for determining a structure of a target biomolecule from crystal data, the method comprising:

(a) employing first computer executable logic to perform multiple molecular replacement searches on crystal data of the target biomolecule using structures of different biomolecules as search models;

(b) employing second computer executable logic to compare the molecular replacement solutions produced by the first computer executable logic in order to predict a biomolecule structure from among the structures with whom the multiple molecular replacement searches were performed whose use as a search model will produce a molecular replacement solution that is superior to the molecular replacement solutions of other biomolecule structures upon which the molecular replacement searches were performed; and

(c) if none of the molecular replacement solutions are comparatively better, evaluating additional biomolecule structures by repeating steps (a) and (b) with the additional biomolecule structures until a biomolecule structure is identified which is predicted to produce a molecular replacement solution that is superior to the molecular replacement solutions of other biomolecule structures upon which the molecular replacement searches were performed.